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Synopsis on

ANALYSIS OF BRAIN IMAGES FOR IDENTIFICATION AND DETECTION OF BRAIN ABNORMALITIES

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Research Topic : **ANALYSIS OF BRAIN IMAGES FOR IDENTIFICATION AND DETECTION OF BRAIN ABNORMALITIES**

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1. Introduction

Diagnosis of Neuro Disorders has always been a challenging area for Medical Science because of the high complexity in the anatomical structure of brain, large variations in size, location and form of the brain tumors and the factors like patient's age, pathological history and symptoms which demand highly specialized skills of the radiologists and the complete clinical examination of the patient. The situation gets critical because of the ever increasing count of the patients suffering from Neuro disorders from year to year throughout the world. It is even worse in developing nations like India where the Radiology group is too small and so is exposed to nearly 3-4 times the number of patients as compared to radiologists of other therefore is exposed to a large number of patients leading to a huge manual workload which is both time consuming and error prone. This makes the automatic brain disorder detection not only desirable but also extremely essential. Over the decade, many methods have been proposed to make tumor segmentation automatic using neural networks, support vector machine (*SVM*), atlas based method, and outlier detection. To obtain satisfactory results a complex prior model or a large amount of training data is required, thus restricting the range of application by the domain of training phase.

2. Literature survey

GLIOMAS are the brain tumors with the highest mortality rate and prevalence. These neoplasms can be graded into Low Grade Gliomas (LGG) and High Grade Gliomas (HGG), with the former being less aggressive and in filtrative than the latter. Even under treatment, patients do not survive on average more than 14 months after diagnosis. Current treatments include surgery, chemotherapy, adiotherapy, or a combination of them.MRI is especially useful to assess gliomas in clinical practice, since it is possible to acquire MRI sequences providing complementary information. The accurate segmentation of gliomas and its intra-tumoral structures is important not only for treatment planning, but also for follow-up evaluations. However, manual segmentation is time-consuming and subjected to inter- and intra-rater errors difficult to characterize. Thus, physicians usually use rough measures for evaluation. For these reasons, accurate semi-automatic or automatic methods are required. However, it is a

challenging task, since the shape, structure, and location of these abnormalities are highly variable. Additionally, the tumor mass effect changes the arrangement of the surrounding normal tissues. Also, MRI images may present some problems, such as intensity inhomogeneity (1), or different intensity ranges among the same sequences and acquisition scanners (2). In brain tumor segmentation, we find several methods that explicitly develop a parametric or non-parametric probabilistic model for the underlying data. These models usually include a likelihood function corresponding to the observations and a prior model. Being abnormalities, tumors can be segmented as outliers of normal tissue, subjected to shape and connectivity constrains. Other approaches rely on probabilistic atlases. In the case of brain tumors, the atlas must be estimated at segmentation time, because of the variable shape and location of the neoplasms. Tumor growth models can be used as estimates of its mass effect, being useful to improve the atlases. The neighborhood of the voxels provides useful information for achieving smoother segmentations through Markov Random Fields (MRF) Zhao also used a MRF to segment brain tumors after a first over segmentation of the image into super voxels, with a histogram-based estimation of the likelihood function. As observed by Menze, generative models generalize well in unseen data, but it may be difficult to explicitly translate prior knowledge into an appropriate probabilistic model. Another class of methods learns a distribution directly from the data. Although a training stage can be a disadvantage, these methods can learn brain tumor patterns that do not follow a specific model. This kind of approaches commonly considers voxels as independent and identically distributed, although context information may be introduced through the features. Because of this, some isolated voxels or small clusters may be mistakenly classified with the wrong class, sometimes in physiological and atomically unlikely locations. To overcome this problem, some authors include information of the neighborhood by Random Field. Classifiers such as Support Vector Machines and, more recently, Random Forests (RF) were successfully applied in brain tumor segmentation. The RF became very used due to its natural capability in handling multi-class problems and large feature vectors. A variety of features were proposed in the literature: encoding context, first-order and fractals-based texture, gradients, brain symmetry, and physical properties. Using supervised classifiers, some authors developed other ways of

applying them. Tustison developed a two-stage segmentation framework based on RFs, using the output of the first classifier to improve a second stage of segmentation. Geremiaet proposed a Spatially Adaptive RF for hierarchical segmentation, going from coarser to finer scales. Meier used a semi-supervised RF to train a subject-specific classifier for post-operative brain tumor segmentation. Other methods known as Deep Learning deal with representation learning by automatically learning a hierarchy of increasingly complex features directly from data. So, the focus is on designing architectures instead of developing hand-crafted features, which may require specialized knowledge. CNNs have been used to win several object recognition and biological image segmentation challenges. Since a CNN operates over patches using kernels, it has the advantages of taking context into account and being used with raw data. In the field of brain tumor segmentation, recent proposals also investigate the use of CNNs.Zikicetal. Used a shallow CNN with two convolutional layers separated by max-pooling with stride3, followed by one fully-connected (FC) layer and a soft max layer. Urban evaluated the use of 3D filters, although the majority of authors opted for 2D filters.3D filters can take advantage of the 3D nature of the images, but it increases the computational load. Some proposals evaluated two-pathway networks to allow one of the branches to receive bigger patches than the other, thus having a larger context view over the image .In addition to their two-pathway network, Havaeietal, Built a cascade of two networks and performed two-stage training, by training with balanced classes and then refining it with proportions near the originals. Lyksborg use a binary CNN to identify the complete tumor. Then, a cellular automata smoothes the segmentation, before a multi-class CNN discriminates the sub-regions of tumor. Rao et al. extracted patches in each plane of each voxel and trained a CNN in each MRI sequence; the outputs of the lastFClayer with soft max of each CNN are concatenated and used to train a RF classifier. Dvorák and Menze divided the brain tumor regions segmentation tasks into binary sub-tasks and proposed structured predictions using a CNN as learning method patches of labels.

Since different brain tumor segmentation methods rely on different image information, : threshold-based methods, which rely on the intensity difference between a brain tumor and surrounding tissues, region-based methods, which search for connected regions of voxels with

similar properties, contour-based methods searching for edges between a brain tumor and surrounding tissues, classification or clustering methods, which make use of voxel-wise intensity and texture features, and atlas-based methods using the prior knowledge about the healthy brain. However, the division is not always clear because proposed methods often have the same nature and combine more of these approaches.

3. Work Done so Far

3.1. Intensity-Based Method

Low-level operations, such as thresholding, edge detection, and morphological techniques, are fast and can be easily adjusted. However, the tumor segmentation performance of these methods highly depends on evident difference in the intensities between tumor and non-tumor regions. Watershed and region growing approaches are simple and consistently produce complete boundaries. However, these two methods are sensitive to noise, which is a common problem in the intensity-based method. Moreover, most intensity-based methods tend to over segment tumors because of the weak and diffused edges caused by edema (3).

3.2. Asymmetry Analysis

The healthy human brain is largely symmetric across the mid-sagittal plane. The asymmetric analysis method for tumor segmentation is based on the principle that tumors, which appear in one of the cerebral hemispheres, can cause asymmetry between the left and right cerebral hemispheres. This asymmetry can be detected, and tumors can be roughly located in the corresponding cerebral hemisphere. The asymmetric analysis method can hasten the tumor detection and segmentation process because tumor segmentation is implemented in one of the cerebral hemispheres. However, accurately finding the mid-sagittal plane is a challenging and time-consuming task. More importantly, asymmetry analysis may not be useful when a tumor is located across the mid-sagittal plane (4).

3.3. Atlas-Based Method

Atlas-based segmentation methods have been extensively investigated. Brain atlases can provide important data prior to tumor segmentation enhancement by measuring the difference

between abnormal and normal brains. However, the deformable registration of the brain atlas to brain images with tumor is an extremely challenging task because of the intensity variations around the tumor caused by edema and the deformations of healthy tissue morphology caused by the tumor mass effect. In a previous study, affine registration is used to align the atlas to the tumor image data. When a large brain structure deformation appears, the misalignment issues are noted on the aligned atlas, which may significantly decrease segmentation accuracy (5).

3.4. Contour/Surface Evolution Method

The contour/surface evolution method has been widely used for the tumor segmentation of 2-D/3-D data. This method can be represented implicitly as a level set function or explicitly as an active contour model/snake function. Compared with the parametric active contour model, the level set method can represent contours with complex topology and handle topological changes, such as splitting and merging in a natural and efficient way. Furthermore, the extension of the level set method to 3D is straight forward and does not require additional machinery .However; the contour/surface evolution method does not easily determine the initializations and tune the parameters even when 3-D level set surfaces are used

3.5. Interactive Algorithm Graph-based seeded segmentation

Framework is one of the popular methods among interactive algorithms. Graph-based seeded segmentation is a global optimization approach, which showed outstanding performance for tumor segmentation in our previous studies. However, this method needs manual seed selection in different tissues, and distinguishing different tissues in the tumor is difficult during the selection of initial seeds for different tissues. In a previous study, a cellular automata-based seeded method, called tumor-cut, has been presented for brain tumor segmentation. This method only requires the user to draw a line over the largest visible tumor diameter. Although this initial seed selection strategy can reduce manual interaction and decrease the sensitivity of the method to initialization, this procedure may not include all tumor areas within the volume of interest along the depth direction, thus leading to tumor under segmentation(6).

3.6. Supervised and Unsupervised Learning Methods

Such as k-means and fuzzy clustering, has become popular for brain tumor segmentation in recent years. The fuzzy method considers that medical images are inherently fuzzy, so it is a very strong tool for medical image processing. Furthermore, the fuzzy method can capture pixel proximity in the same objective region without a training step. However, most fuzzy methods work well only for tumors that present hyper-intensity and exhibit poor performance on segmenting non enhanced tumors(7). These conditions are due to the fact that these fuzzy methods typically use intensity-based method, such as thresholding and morphological operations, as pre- or post-processing.

Supervised classification learning method is widely used in tumor segmentation. Well-trained classifiers can extract discriminative information from the training data and estimate the label of each voxel in a testing volume. However, the traditional classification methods classify each voxel into different classes without considering the spatial correlation between current and nearby voxels. This method may not obtain a global optimized result. To address this problem, a classification method is generally combined with a regularization step. The regularization step can be implemented by modeling the boundary or by applying a variant of a random field spatial prior (MRF/CRF). In the previous studies, context-aware spatial features and the probabilities obtained by tissue-specific Gaussian mixture models are used as inputs for classifiers, and satisfied segmentation results are achieved without using posthoc regularization. Novel classification method, named local independent projection-based classification (LIPC), for brain tumor segmentation without using explicit regularization(6).

4.Results of Existing Methodologies

Table 1. Data Sets, MR Image Modalities, Evaluation Score and even Tumor Types Used in Self-Reported Performance in the Brain Tumor Segmentation Literature Differ Widely.

Algorithm	MRI Modalities	Approach	Perform. Score	Tumor Type	Training/Testing tt/cv
Fletcher 2001	T1 T2 Pd	Fuzzy Clustering / Image Retrieval	Match (53-91%)	na	2/4 tt
Kaus 2001	T1	Template-Moderated Classification	Accuracy (95%)	LG , M	10/10 tt
Ho 2002	T1 T1c	Level Sets/Region Competition	Jaccard (85-93%)	G,M	na/5 tt
Prastawa 2004	T2	Generative Model/Outlier Detection	Jaccard (59-89%)	G,M	na/3 tt
Corso 2008	T1 T1c T2 FLAIR	Weighted Aggregation	Jaccard (62-69%)	HG	10/10 tt
Varma 2008	T1 T1c T2 FLAIR DT1	SVM	Accuracy (34-93%)	HG	14/14 cv
Wels 2008	T1 T1c T2	Discriminative Model /CRF	Jaccard (78%)	G	6/6 cv
Cobzas 2009	T1C FLAIR	Level/CRF	Jaccard (50-75%)	G	6/6 tt
Wang 2009	T1	Fluid Vector Flow	Tanimoto (60%)	na	0/10 tt
Menze 2010	T1 T1c T2 FLAIR	Generative Model/Lesion Class	Dice (40-70%)	G	25/25 cv
Baucer 2011	T1 T1c T2 FLAIR	Hierarchical SVM/CRF	Dice (77-84%)	G	10/10 cv

Table2. Overview of Algorithms

Method	Description	Fully Automated	Year
Bauer	Integrated hierarchical random forest classification and CRF regularization	Yes	2012
Geremia	Spatial decision forests with intrinsic hierarchy	Yes	2012
Hamamci	Tumor cut method	No	2012
Menze(G)	Generative lesion segmentation model	Yes	2012
Menze(D)	Generative discriminative model building on the top of the Menze G	Yes	2012
Riklin Raviv	Generative model with latent atlases and level sets	No	2012
Shin	Hybrid clustering and classification by logistic regression	Yes	2012
Subbanna	Hierarchical MRF approach with Gabor features	Yes	2012
Zhao	Learned MRF on super voxels clusters	Yes	2012
Zikic	Context sensitive features with decision tree ensemble	Yes	2012
Buendia	Bit grouping artificial immune network	Yes	2013
Cordier	Patch based tissue segmentation approach	Yes	2013
Doyle	Hidden Markov fields and variational EM in a generative model	Yes	2013
Festa	Random forest classifier using neighborhood and local context features	Yes	2013
Guo	Semiautomatic segmentation using active contours	No	2013
Meier	Appearance and context sensitive features with random forest and CRF	Yes	2013
Reza	Texture features and random forests	Yes	2013
Taylor	“Map reduce enabled” Hidden Markov models	Yes	2013
Tustison	Random forest classifier using the open source ANTs/ANTsR packages	Yes	2013
Zhao(ii)	Like Zhao(i) with updated unary potential	Yes	2013

5. Imaging Modalities

Along with the advance of medical imaging, imaging modalities play an important role in the evaluation of patients with brain tumors and have a significant impact on patient care. Recent years, the emerging new imaging modalities, such as X-ray, Ultra sonography, Computed Tomography (CT), Magneto Encephalo Graphy (MEG), Electro Encephalo Graphy (EEG), Positron Emission Tomography (PET), Single-Photon Emission Computed Tomography (SPECT), and Magnetic Resonance Imaging (MRI), not only show the detailed and complete aspects of brain tumors, but also improve clinical doctors to study the mechanism of brain tumors at the aim of better treatment. Clinical doctors play an important role in brain tumor assessment and therapy. Once a brain tumor is clinically suspected, radiologic evaluation is required to determine the location, the extent of the tumor, and its relationship to the surrounding structures. This information is very important and critical in deciding between the different forms of therapy such as surgery, radiation, and chemotherapy. Therefore, the evaluation of brain tumors with imaging modalities is now one of the key issues of radiology departments. MRI is a non-invasive and good soft tissue contrast imaging modality, which provides invaluable information about shape, size, and localization of brain tumors without exposing the patient to a high ionization radiation. MRI is attracting more and more attentions for the brain tumor diagnosis in the clinical .Incurrent clinical routines, the images of different MRI sequences are employed for the diagnosis and delineation of tumor compartments.

These sequence images include

1) T1-weighted MRI (T1w)

2) T1-weighted MRI with contrast enhancement (T1wc)

3) T2-weighted MRI (T2w)

4) Proton Density-weighted MRI (PDw),

5) Fluid Attenuated Inversion Recovery (FLAIR)

Figure 1 shows an axial slice of four standard sequences for a glioblastoma (a type of brain tumor) patient. Since T1w allows for an easy annotation of the healthy tissues, it has become the most commonly used sequence images for the brain tumor structure analysis. Moreover,

T1-weighted contrast-enhanced sequence images can make the brain tumor borders become brighter because the contrast agent accumulates there due to the disruption of the blood-brain barrier in the proliferative brain tumor region. In these sequence images, the necrotic core and the active cell region can be distinguished easily. In T2w, the edema region can appear brighter than other sequence images of MRI. Since the signal of water molecules is suppressed in the imaging process of FLAIR, FLAIR is regarded as a highly effective sequence image to help separate the edema region from the CSF (6).

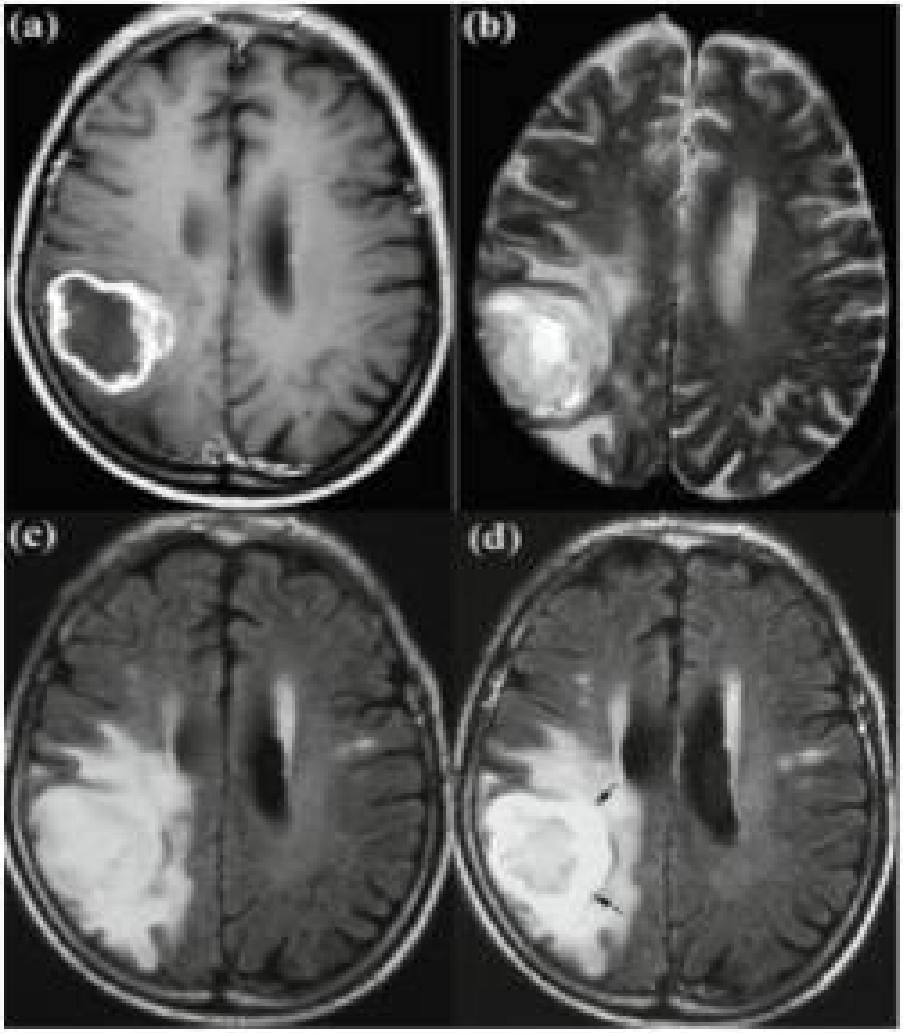

Fig. 1 Four imaging modalities: (a) T1-weighted MRI; (b) T2-weighted MRI; (c) FLAIR; and (d) FLAIR with contrast enhancement[5].

6. Proposed Methodology and Further Work

6.1 Challenges Identified for Further work

1) Feature extraction for brain tumor: New features can be designed to obtain better results. This could improve the accuracy, validity, and robustness of MRI-based brain tumor segmentation (8).

2) Multimodal images: This would increase the quality of the overall segmentation results (14).

3) Classification of detected tumor (12).

4) Segmentation of the tumor active core region (9).

5) Skull-stripping approach: For early detection of autism.

6) Identification of the tumors of the very small, less detailed and overlapping regions of brain (13).

7) To develop better Segmentation algorithms and higher MR sequences: This could decrease the number of false negative cases (10)

8) Fusion of different segmenters: This could improve performance of detection of tumor significantly.

9) Methods to avoid over segmentation (11).

6.2 Proposed Method

• Simulation: – Verification of existing methods and newly design methods via simulation in MATLAB-Simulink tool.

• Validation: 1) Implementation of proposed method on actual setup of laboratory.

2) Comparative study of existing method and proposed method. – Comparison of simulated results and implemented results for particular case.

Three major steps for this concept

1) Pre-processing

2) Classification

3) Post processing.

7. Proposed Method Title

"Brain Image Analysis for Identification and Detection of Brain Abnormalities "

Objective of Method

To develop a fully automatic brain abnormalities detection method with minimum running time along with noise removal, boundary detection, and to develop best segmentation methodology comparing with existing systems.

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